

Sequence Listing

SEQ ID NO. 1 - The full-length nucleotide sequence of the spike (S) gene of SARS CoV, clone 12 of 2774 strain

RNA linear

ORGANISM: SARS coronavirus 2774 strain

Viruses; ssRNA positive-strand viruses, no DNA stage;
Nidovirales; Coronaviridae; Coronavirus.

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 acaca 3765

SEQ ID NO. 2 - The full-length amino acid sequence of the spike (S)
 gene of SARS CoV, clone 12 of 2774 strain
 Amino acid

1 MFIFLLFLTL TSGSDLDRCT TFDDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLSTL
 PFYSNVTGFH 70
 71 TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS TNVIRACNF
 ELCDNPFPAV 140
 141 SKPMGTQHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK HREFVFKNK DGFLVYKGY
 QPIDVVRDLP 210
 211 SGFNTLKPFI KLPLGINITN FRILTAFSP AQDIWGTSAAYFVGDLPKT TFMLKYDENG
 TITDAVDCSQ 280
 281 NPLAELKCSV KSFEIDKGIY QTSNFRVVPV GDVVRFPNIT NLCPFGEVEN ATKFPSVYAW
 ERKKISNCVA 350 351 DYSVLNSTV FSTFKCYGVS ATKLNLCFS NVYADSFVVK GDDVRQIAPG
 QTGVADIYNY KLPDDFMGCV 420 421 LAWNTRNIDA TSTGNVYKY RYLRHGKLRP FERDISNVFP
 SPDGKPCPTP ALNCYWPLND YGFYTTTGIG 490 491 QPYRVVLS FELNAPATV CGPKLSTDLI
 KNQCVNFNFN GLTGTGLVLP SSKRFQFFQ FGRDVSDFD 560 561 SVRDPKTSEI LDISPCFSGG
 VSVITPGTNA SSEAVLYQD VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ 630 631 TQAGCLIGAE
 HVDTSYECDI PIGAGICASY HTVSLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF 700 701
 SISITTEVMP VMAKTSVDC NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM
 770 771 YKTPTLKYFG GFNFSQILPD PLKPTKRSFI EDLLFNKVTI ADAGFMKQYG ECLGDINARD

LICAQKFNGL 840 841 TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRENG
 IGVTONVLYE NQKQIANQFN 910 911 KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS
 NFGAISSVLN DILSRDKVE AEVQIDRLIT 980 981 GRLQSLQTYV TQQLIRAAEI RASANLAATK
 MSECVLGQSK RVDFCGKGYH LMSFPQAAPH GVVFLHVTYA 1050 1051 PSQERNFTTA PAICHEGKAY
 FPREGVFVFN GTSWFITQRN FFSPQIITD NTFVSGNCDV VIGIINNTVY 1120
 1121 DPLQPELDSF KEELDKYFKN HTSPDVLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI
 DLQELGKYEQ 1190 1191 YIKWPWYVWL GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE
 DDSEPVKGV KLHYT 1255

SEQ ID NO. 3 - The nucleotide sequence of SA10 fragment of the spike
 (S) gene of SARS CoV, clone 12 of 2774 strain

3087 taccacctta tgccttccc acaagcagcc ccgcatggtg ttgtcttctt acatgtcacg
 tatgcgccat 3157 3158 cccaggagag gaacttcacc acagcgccag caatttgta tgaaggcaaa
 gcatacttcc ctcgtgaagg 3227 3228 tgtttttggg tttaatggca cttcttggtt tattacacag
 aggaacttct tttctccaca aataattact 3297 3298 acagacaata catttgcttc aggaaattgt
 gatgtcggtta ttggcatcat taacaacaca gtttatgatc 3367 3368 ctctgcaacc tgagcttgac
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 3577
 3578 tta
 3581

SEQ ID NO. 4 - The amino acid sequence of SA10 fragment of the spike
 (S) gene of SARS CoV, clone 12 of 2774 strain

1029 YHLSFPQAA PHGVVFLHVT YAPSQERNFT TAPAICHEGK AYFPREGVFV FNGTSWFITQ
 RNFFSPQIIT 1099 1100 TDNTFVSGNC DVVIGIINNT VYDPLQPELD SFKEELDKYF KNHTSPDVL
 GDISGINASV VNIQKEIDRL 1169 1170 NEVAKNLNES LIDLQELGKY EQYI
 1192

SEQ ID NO. 5 - The amino acid sequence of the neutralizing fragment
 of the spike (S) gene of SARS CoV, clone 12 of 2774 strain

1055 RNFT TAPAICHEGK AYFPREGVFV FNGTSWFITQ RNFFSPQIIT TDNTFVSGNC DVVIGIINNT
 VYDPLQ 1620 1621 PELDSFKEELDKYF KNHTSPDVL GDISGINASV VNIQKEIDRL NEVAKNLNES
 LIDLQELGKY EQYI 1192

SEQ ID NO. 6 - The amino acid sequence of SA11 fragment of the spike
 (S) gene of SARS CoV, clone 12 of 2774 strain

1 MFIFLLFLTL TSGSDLDRCT TFDDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLNL
 PFYSNVTGFH 70
 71 TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFSGTMNNK SQSVIIINNS TNVVIRACNF
 ELCNPFPAV 140
 141 SKPMGTQHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK HLREFVFNK DGFLYVYKGY
 QPIDVVRDLP 210

211 SGFNTLKPIF KLPLGINITN FRAILTAFSP AQDIWGTSA A YFVGD LKPT TFMLKYDENG
TITDAVDCSQ 280

281 NPLAELKCSV KSFEIDKGIY QTSNFRV VPS GDVVRFPNIT NLCPFGEVEN ATKFPSVYAW
ERKKISNCVA 350 351 DYSVLYNSTV FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG
QTGVIADYNY KLPDDFMGCV 420 421 LAWNTRNIDA TSTGNYNKY RYLRHGKLRP FERDISNVPF
SPDGKPCTPP ALNCYWPLND YGFYTTTGIG 490 491 YQPYRVVLS FELLNAPATV CGPKLSTDLI
KNQCVNFNFN GLTGTGVLTP SSKRFQPFQ FGRDVSDFTD 560 561 SVRDPKTSEI LDISPCSFGG
VSVITPGTNA SSEVAVLYQD VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ 630 631 TQAGCLIGAE
HVDTSYECDI PIGAGICASY HTVSLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF 700 701
SISITTEVMP VSMAKTSVDC NMYICGDSTE CANLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM
770 771 YKTPTLKYFG GFNFSQILPD PLKPTKRSFI EDLLFNKVTI ADAGFMKQYG ECLGDINARD
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NFGAISSVLN DILSRDLKVE AEVQIDRLIT 980 981 GRLOSLQTYV TQQLIRAAEI RASANLAATK
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FPREGVFVFN GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY 1120

1121 DPLQPELDSF KE

1132